

Fig.1

SEQ ID NO: 12

1 GAATTCATGG TGTTTGATC ATTTAAATT TTTATATGGC GGGTGGTGGG CAACTCGCTT 60
60 CGGGGCAACT CGCTTACCGA TTACGTTAGG GCTGATATT ACGTAAAAAT CGTCAAGGGA 120
121 TGCAAGACCA AAGTAGTAAA ACCCCGGAGT CAACAGCATC CAAGCCCAAG TCCTTCACGG 180
181 AGAAACCCA GCGTCCACAT CACGAGCGAA GGACCACCTC TAGGCATCGG ACGCACCATC 240
241 CAATTAGAAG CAGCAAAGCG AAACAGCCA AGAAAAAGGT CGGCCCGTCG GCCTTTCTG 300
301 CAACGCTGAT CACGGGCAGC GATCCAACCA ACACCCTCCA GAGTGACTAG GGGCGGAAAT 360
361 TTAAAGGGAT TAATTCCAC TCAACCACAA ATCACAGTCG TCCCCGGTAT TGTCCCTGCAG 420
421 AATGCAATT AAACCTTTCT GCGAATCGCT TGGATTCCCC GCCCCTGGCC GTAGAGCTTA 480
481 AAGTATGTCC CTTGTCGATG CGATGTATCA CAACATATAA ATACTAGCAA GGGATGCCAT 540
541 GCTTGGAGGA TAGCAACCGA CAACATCACA TCAAGCTCTC CCTTCTCTGA ACAATAAAC 600
601 CCACAGAAGG CATT 615

Fig. 1 O

The diagram illustrates the SRE sequence as a horizontal line with three black boxes representing transcription start sites. A dotted arrow points from the first two boxes to the sequence CGGAAATTAAAGG, which is labeled SEQ ID NO: 6. Another dotted arrow points from the first two boxes to the sequence CGGAAATTAAACGG, which is labeled SEQ ID NO: 8. A third dotted arrow points from the first two boxes to the sequence CGGAAATTAAATA, which is labeled SEQ ID NO: 30. An arrow points from the sequence CGGAAATTAAAGG to the gene taaP. An arrow points from the sequence CGGAAATTAAACGG to the gene taaS. An arrow points from the sequence CGGAAATTAAATA to the gene MSRE2.

	SRE sequence		Amylase Activity (U/g dry mycelia) (ratio)	
SEQ ID NO: 6	CGGAAATTAAAGG	taaP	1041	1
SEQ ID NO: 8	CGGAAATTAA <u>AC</u> GG	taaS	1209	1.2
SEQ ID NO: 30	CGGAAATTAA <u>AT</u> A	MSRE2	792	0.8